

OY		3	ASSDPELVDDGG-----DNIPRELRKRGCTHYMTNGSINSSHHLLDLDEPI	52
Dd		22	ASDDEL--LDGAGVIMDFOTISEDNL-LDGDTAVGTHITMNGSINSSTHLLDLDEPI	79
OY		53	PVGVTGYDDFHTIDWVREKCKDRERHRIRNSKKKSASAMDMTKSLVDANSGLVLTGLAS	112
Dd		80	PGCVGTYYDDFHTIDWVREKCKDRERHRIRNSKKKSASAMDMTKSLVDANSGLVLTGLAS	139
OY		113	GALAGLLDIADMMTDLKEGICLSALWYNHOCCWGSNETTFEERDKCPOMKIWAELIIG	172
Dd		140	GALAGLLDIADMMTDLKEGICLSALWNHQCCWGSNETTFEERDKCPOMKIWAELIIG	199
OY		173	QAEGGSYIMMYIMYIFMALSFPAFLASLYVFAPYACSGSIPKIKTLISGIIRGLK	232
Dd		200	QAEGGSYIMMYIMYIFALSFAFLASLYVFAPYACSGSIPKIKTLISGIIRGLK	259
OY		233	WTLMKTITLVLAAVAGSLCKEGRLVHVACCNGNIFYLPKYSTNEARKREVLSASA	292
Dd		260	WTLMKTITLVLAAVAGSLCKEKRPVLHVACCNNIFYLPKYSTNEARKREVLSASA	319
OY		293	AGVSATFAPRIGGVLFSEESYSYPPLKTRSPFALVAFYRSINPGRSRIYLFEV	352
Dd		320	AGVSATFAPRIGGVLFSEESYSYPPLKTRSFALVAFYRSINPGRSRIYLFEV	379
OY		353	EYHPWYLELPEPLLGEFGGLMGAFETRANIAMCRKRSTKGXYPLEVIIVAITA	412
Dd		380	EYHPWYLELPEPLLGEFGGLMGAFETRANIAMCRKRSTKGXYPLEVIIVAITA	439
OY		413	VIAFPNPYTRLNTSELKRELTPDCGPRESSSLCDYRDNMASKIVDIPDRPAGICYSA	472
Dd		440	VIAFPNPYTRLNTSELKRELTPDCGPRESSSLCDYRDNMASKIVDIPDRPAGICYSA	499
OY		473	IWOCLALIFKIMTVFTFGIKVPSGFLFISMAIGATRIGVIAEQOLAYVHHDMFIK	532
Dd		500	IWOCLALIFKIMTVFTFGIKVPSGLFPSMAIGATRIGVIAEQOLAYVHHDMFIK	559
OY		533	EMCEYGACCTPPGLXAWYGAACCGVYTRMTVSLVYVEFELTGLEYVLAAMVMTSKY	592
Dd		560	EMCEYGACCTPPGLXAWYGAACCGVYTRMTVSLVYVEFELTGLEYVLAAMVMTSKY	619
OY		593	VGDFAFGREGIYEANI RLNGYFPFLDAKEEFHTTYLAADVMPRRNDPLAVLTODNNMTVD	652
Dd		620	VGDFAFGREGIYEANI RLNGYFPFLDAKEEFHTTYLAADVMPRRNDPLAVLTODNNMTVD	679
OY		653	IENMINETSYNGFPVIMSKEQSRLVGFALRDLTIAESARKKOEGIVGSSRVCFQAQHP	712
Dd		680	IENMINETSYNGFPVIMSKEQSRLVGFALRDLTIAESARKKOEGIVGSSRVCFQAQHP	739
OY		713	SLEPASPEPLKRSILDSPTVYDHPMEIVDIEFKLRLCQLVTHNRLLGITTKKD	772
Dd		740	SLEPASPEPLKRSILDSPTVYDHPMEIVDIEFKLRLCQLVTHNRLLGITTKKD	799
OY		773	ILRHMAQTANODPASIMFN 791	
Dd		800	ILRHMAQTANODPASIMFN 818	
RESULT 2				
		Q9R287		
ID	Q9R287	PREDIMINARY:	PRT:	818 AA.
AC	Q9R287			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Chloride channel protein 3 long form (Fragment).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY;			
IX	MEDLINE=20378002; PubMed=10915634;			

Query Match	Best Local Similarity	Score	DB	Length
3 ASSDPLPDPDGG-----DNIPRLREKRCRTHYTMNGGINSSTHLLDDEPT	96.5%	4032	DB 11	818
22 ASSDEEL-LDGGALIMDPQTSDDNL-LDGDYAACTHTMTNGGINSSTHLLDDEPT	96.7%	3318	DB 12	818
53 PGVGYDDEFTIDWYREKCKDRRRRRINSKKESAMEKTSKYAAMGMLVLTGLAS	96.7%	3318	DB 13	818
80 PGVGYDDEFTIDWYREKCKDRRRRRINSKKESAMEKTSKYAAMGMLVLTGLAS	96.7%	3318	DB 14	818
113 GALAGIDIDAAWMMDLKEGICLSALWNBHCCGSGNETTEERDKCPQMTMELIIG	96.7%	3318	DB 15	818
140 GALAGIDIDAAWMMDLKEGICLSALWNBHCCGSGNETTEERDKCPQMTMELIIG	96.7%	3318	DB 16	818
173 OAEFGSYIMNYIMYIFWALSFALAVSLVYFADYACGSGIPEIKTILSGFIRGYLCK	96.7%	3318	DB 17	818
200 OAEFGSYIMNYIMYIFWALSFALAVSLVYFADYACGSGIPEIKTILSGFIRGYLCK	96.7%	3318	DB 18	818
233 WTLMTKTTILVAVASGLSGKEGSLVYACCGNIFSTLPKYSTNEAKKREVLASASA	96.7%	3318	DB 19	818
260 WTLMTKTTILVAVASGLSGKEGSLVYACCGNIFSTLPKYSTNEAKKREVLASASA	96.7%	3318	DB 20	818
293 AGVSAFAGPAGIGVLESEVSYPEPLKTLMSRFFAALVAAFLVLSINDFGNSRLVLEFV	96.7%	3318	DB 21	818
320 AGVSAFAGPAGIGVLESEVSYPEPLKTLMSRFFAALVAAFLVLSINDFGNSRLVLEFV	96.7%	3318	DB 22	818
353 EYHTWYLFELFPFLLGLVFGGJLMAFFIRANIAMCRKRKSTKPKYPLEVIYAAITA	96.7%	3318	DB 23	818
380 EYHTWYLFELFPFLLGLVFGGJLMAFFIRANIAMCRKRKSTKPKYPLEVIYAAITA	96.7%	3318	DB 24	818
413 VIAPFNPTRLNLSLIELFTDCGPLLESSLCDYRNDNMASKIYDDIPDRAGIGVSA	96.7%	3318	DB 25	818
440 VIAPFNPTRLNLSLIELFTDCGPLLESSLCDYRNDNMASKIYDDIPDRAGIGVSA	96.7%	3318	DB 26	818
473 IWOLCLALFKIIMTVFTFGIKVPSGLFIPSMAGIALGRIAGIYIAVEOLAVYHHDMFTFK	96.7%	3318	DB 27	818
500 IWOLCLALFKIIMTVFTFGIKVPSGLFIPSMAGIALGRIAGIYIAVEOLAVYHHDMFTFK	96.7%	3318	DB 28	818
533 EMCCEVAGCIPPGGLVAMGAACGLGVRMTVSLVVIYFELTGLGEIYIYPLMAAAMTSKW	96.7%	3318	DB 29	818
560 EMCCEVAGCIPPGGLVAMGAACGLGVRMTVSLVVIYFELTGLGEIYIYPLMAAAMTSKW	96.7%	3318	DB 30	818
593 VGDAFGREGIYEAHIRLNGYFPLDAKKEEFTHTTLAADYMRPRRNDPPLAVLITQDMMTYDD	96.7%	3318	DB 31	818
620 VGDAFGREGIYEAHIRLNGYFPLDAKKEEFTHTTLAADYMRPRRNDPPLAVLITQDMMTYDD	96.7%	3318	DB 32	818
653 IENMINEYSYNGEPVIMSKESORLVGFALRDLTIAISARKKOGCIYSSSVCAQHTP	96.7%	3318	DB 33	818
660 IENMINEYSYNGEPVIMSKESORLVGFALRDLTIAISARKKOGCIYSSSVCAQHTP	96.7%	3318	DB 34	818
713 SLPAESPRLKRLSLDMSPTVDTHTMEIYVDIFRKLGLRQCLVTHNGRLGLITTKKD	96.7%	3318	DB 35	818
740 SLPAESPRLKRLSLDMSPTVDTHTMEIYVDIFRKLGLRQCLVTHNGRLGLITTKKD	96.7%	3318	DB 36	818
773 ILRHMAQTANODPASIMFN 791	96.7%	3318	DB 37	818
800 ILRHMAQTANODPASIMFN 818	96.7%	3318	DB 38	818

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RESULT 3
ID 018894 PRELIMINARY; PRT; 760 AA.
AC 018894;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Chloride channel protein 3 (CLC-3).
GN CLCN3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=CORNEAL ENDOTHELIUM;
RA Rae J.L., Shepard A.R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL
CC CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
CC PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
CC TERM MEMORY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER CHLORIDE CHANNELS.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
DR EMBL: AF029348; AAB95163.1; ALT_INIT.
DR InterPro: IPR000644; CBS_domain.
DR pfam: PF005711; CBS; 2.
DR pfam: PF00654; voltage_clc; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 202 222 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
FT TRANSMEM 285 305 POTENTIAL.
FT TRANSMEM 330 350 POTENTIAL.
FT TRANSMEM 365 385 POTENTIAL.
FT TRANSMEM 442 462 POTENTIAL.
FT TRANSMEM 467 487 POTENTIAL.
FT TRANSMEM 508 528 POTENTIAL.
FT TRANSMEM 536 556 POTENTIAL.
FT DOMAIN 577 616 CBS 1.
FT DOMAIN 698 749 CBS 2.
SO SEQUENCE 760 AA; 84516 MW; 9B6DDA86296847E7 CRC64;

Query Match 95.8%; Score 4002; DB 6; Length 760;
Best Local Similarity 100.0%; Pred. No. 8.8e-316;
Matches 760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 181 SGPEIKTIIISGFIIRGYICKMTIMKTITLVAVASGLSLGKEGPIVHVHACCCGNFSY 240
OY 272 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSEBVSYPPLKTLMSRFALV 331
DB 241 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSEBVSYPPLKTLMSRFALV 300
OY 332 AAFVLSINPFGNSRLVLEYVHTPWYLFELPFIILGVFGILMGAFPIRANIAMCRRR 391
DB 301 AAFVLSINPFGNSRLVLEYVHTPWYLFELPFIILGVFGILMGAFPIRANIAMCRRR 360
OY 392 KSKFKGKYPVLEVYIVAVIAFAFPPYRRLNSELIRKELFDGGLSSSLCDYRNDM 451
DB 361 KSKFKGKYPVLEVYIVAVIAFAFPPYRRLNSELIRKELFDGGLSSSLCDYRNDM 420
OY 452 NASKIVDIPDRPAGIGVSAIMOLCLALFKIIMVTFPGIKVPSGLFIPSMAGIAG 511
DB 421 NASKIVDIPDRPAGIGVSAIMOLCLALFKIIMVTFPGIKVPSGLFIPSMAGIAG 480
OY 512 RIVGIAEOLAYYHHDFIEKWCCEVGADCTTPGLYAMVGAACLGVTMTVSLVIVF 571
DB 481 RIVGIAEOLAYYHHDFIEKWCCEVGADCTTPGLYAMVGAACLGVTMTVSLVIVF 540
OY 572 ELVGLEYIVPMAAVMTSKWGDAPRGEGIYEAHIRPLNGYPIFDAKEETHHTLADVM 631
DB 541 ELVGLEYIVPMAAVMTSKWGDAPRGEGIYEAHIRPLNGYPIFDAKEETHHTLADVM 600
OY 632 RPRRNDPPLAVLQDNTVDIDIEMINETSYNGPVTMSKESOLVGFALRDLTIAES 691
DB 601 RPRRNDPPLAVLQDNTVDIDIEMINETSYNGPVTMSKESOLVGFALRDLTIAES 660
OY 692 ARKKQEGIVSSRVCEQAHTPSPAPESRPLKLSILDMSPFTVTDHTPEIIVDIFRKL 751
DB 661 ARKKQEGIVSSRVCEQAHTPSPAPESRPLKLSILDMSPFTVTDHTPEIIVDIFRKL 720
OY 752 GLRQCLVTHNGRLIGITTKRDLIRHMAQTANODPASTMEN 791
DB 721 GLRQCLVTHNGRLIGITTKRDLIRHMAQTANODPASTMEN 760

RESULT 4
OY0YH11 PRELIMINARY; PRT; 791 AA.
ID 0Y0YH11;
AC 0Y0YH11;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Putative chloride channel CLC-3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DISTAL NEPHRON;
RA Lindenthal S.M.B.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y09941; CAAT1072.2; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl_channel_volt.
DR pfam: PF005711; CBS; 2.
DR pfam: PF00654; voltage_clc; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
SO SEQUENCE 791 AA; 88140 MW; 216B1B1ED2A8C4EA CRC64;

Query Match 95.6%; Score 3993; DB 13; Length 791;
Best Local Similarity 94.2%; Pred. No. 5e-315;
Matches 745; Conservative 26; Mismatches 20; Indels 0; Gaps 0;
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QY 61 FHTIDWREKCKDBRRHRINSKSKESAMEMTKSLYDAMSGMLVLTGLASGALAGLID 120
DB 61 FHTIDWREKCKDBRRHRINSKSKESAMEMTKSLYDAMSGMLVLTGLASGALAGLID 120
QY 121 IADWMTDLKKGICLSALWYHNEOCCWGSNETTEERDKCPQWKTWAEILIGQAGPGSY 180
DB 121 IADWMTDLKKGICLSALWYHNEOCCWGSNETTEERDKCPQWKTWAEILIGQAGPGSY 180
QY 181 IMNYIMYEMALSFAPLAVSLVKYFAPAGSGIPEIKITISGFIIRGYLCKWTLMTITI 240
DB 181 IMNYIMYEMALSFAPLAVSLVKYFAPAGSGIPEIKITISGFIIRGYLCKWTLMTITI 240
QY 241 TLVLAVASGLSGKEGRLVHVACCCGNIFSYLFPKYSTNEAKKREVLASAAGSVAFG 300
DB 241 TLVLAVASGLSGKEGRLVHVACCCGNIFSYLFPKYSTNEAKKREVLASAAGSVAFG 300
QY 301 APIGGVLSLEEVSYFPLKTLKMSRFPALVAAYLKSINFGNSRLVLFVEYHTPYL 360
DB 301 APIGGVLSLEEVSYFPLKTLKMSRFPALVAAYLKSINFGNSRLVLFVEYHTPYL 360
QY 361 FELPPEILGFGGIMGAFIRANIAMCRKSKFGKYPVLEVIYVAITAVIAFPNRY 420
DB 361 FELPPEILGFGGIMGAFIRANIAMCRKSKFGKYPVLEVIYVAITAVIAFPNRY 420
QY 421 TRLMTSELKELFTDCGPLESSSLCDYRNDMNASKIYDDIPDRAGIGVSAIMQLAL 480
DB 421 TRLMTSELKELFTDCGPLESSSLCDYRNDMNASKIYDDIPDRAGIGVSAIMQLAL 480
QY 481 IEKIMIVFTGIVPGLSFLPISMAIGALAGRTYGLAEQOLAYHHDMFIREKCEVAD 540
DB 481 IEKIMIVFTGIVPGLSFLPISMAIGALAGRTYGLAEQOLAYHHDMFIREKCEVAD 540
QY 541 CITPGLIYAMGAACLGVTMTSLVYIVFELTGGLEYIYPLMAAVTSMWGDAGRE 600
DB 541 CITPGLIYAMGAACLGVTMTSLVYIVFELTGGLEYIYPLMAAVTSMWGDAGRE 600
QY 601 GIYFAHIRLNGYPLDAKEEFTHTTLADYMRPRNDPPLAVLTQDMNTVDIENMINET 660
DB 601 GIYFAHIRLNGYPLDAKEEFTHTTLADYMRPRNDPPLAVLTQDMNTVDIENMINET 660
QY 661 SYNEPPLVMSKESORLNGFALRDLTIAESARKKOEIVSSRVCFAQHPSPSPAESPR 720
DB 661 SYNEPPLVMSKESORLNGFALRDLTIAESARKKOEIVSSRVCFAQHPSPSPAESPR 720
QY 721 PLKRLSILMSPTVTDHTPMEIYVDIFRKILGRLQCLVTHNGRLGIIITKKDILRHMAQT 780
DB 721 PLKRLSILMSPTVTDHTPMEIYVDIFRKILGRLQCLVTHNGRLGIIITKKDILRHMAQT 780
QY 781 ANODPASIMFN 791
DB 781 ANHDPESILFN 791

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RESULT 5
P97274 PRELIMINARY; PRT: 760 AA.
ID P97274
AC P97274
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-MAY-1999 (TEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Volume-regulated outwardly-rectifying chloride channel.
GN CLC-3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
ON NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049352; Pubmed=9389484;
RA Duan D., Winter C., Cowley S., Hume J.R., Horowitz B.;
RT "Molecular identification of a volume-regulated chloride channel.";
RL Nature 390:417-421(1997).

RN [2]
 RP SEQUENCE FROM N.A.
 RA Duan D., Winter C., Hume J.R., Horowitz B.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U83464; AAB88634.2;
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001807; Cl-channel_volt.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00654; voltage_CLC; 1.
 DR PRINTS: PR00762; CLCHANNEL.
 DR SMART: SM00116; CBS; 2.
 SQ SEQUENCE 760 AA; 84357 MW; DE8D017D1881A531 CRC64;

Query Match 95.4%; Score 3984; DB 11; Length 760;
 Best Local Similarity 99.6%; Pred. No. 2,5e-314;
 Matches 757; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 32 MTNGSINSSTHLLDLDEPIPGVGYDDFTIDWREKCKDBRRHRINSKSKESAMEM 91
DB 1 MTNGSINSSTHLLDLDEPIPGVGYDDFTIDWREKCKDBRRHRINSKSKESAMEM 60
QY 92 TKSLYDAMSGMLVLTGLASGALAGLIDADWMTDLKKGICLSALWYHNEOCCWGSNE 151
DB 61 TKSLYDAMSGMLVLTGLASGALAGLIDADWMTDLKKGICLSALWYHNEOCCWGSNE 120
QY 152 TTFEERDKCPQWKTWAEILIGQAGPGSYIMNYIMYEMALSFAPLAVSLVKVAPYACG 211
DB 121 TTFEERDKCPQWKTWAEILIGQAGPGSYIMNYIMYEMALSFAPLAVSLVKVAPYACG 180
QY 212 SGIEPIKITLSGFIIRGYLCKWTLMTITIVLAVASGLSGKEGRLVHVACCCGNIFSY 271
DB 181 SGIEPIKITLSGFIIRGYLCKWTLMTITIVLAVASGLSGKEGRLVHVACCCGNIFSY 240
QY 272 LFPKYSTNEAKKREVLASAAGSVAFGAPIGVLSLEEVSYFPLKTLKMSRFPALV 331
DB 241 LFPKYSTNEAKKREVLASAAGSVAFGAPIGVLSLEEVSYFPLKTLKMSRFPALV 300
QY 332 AAFVLRISINPGNSRLVLFVEYHTPYLFEPLPPEILGFGGIMGAFIRANIAMCR 391
DB 301 AAFVLRISINPGNSRLVLFVEYHTPYLFEPLPPEILGFGGIMGAFIRANIAMCR 360
QY 392 KSTFGKYPVLEVIYVAITAVIAFPNRYTRLNLSLKELEFTCCGPLESSSLCDYRDM 451
DB 361 KSTFGKYPVLEVIYVAITAVIAFPNRYTRLNLSLKELEFTCCGPLESSSLCDYRDM 420
QY 452 NASKIYDDIPDRPAGVGYSAIMQLCLALFKIIMYVFTGIRKPSGLFIPSMALGALAG 480
DB 421 NASKIYDDIPDRPAGVGYSAIMQLCLALFKIIMYVFTGIRKPSGLFIPSMALGALAG 480
QY 512 RIVGIAVEQLAYHHDMFIREKCEVAGADCTTGPLYAMVGAACLGVTMTVSLVYIVF 571
DB 481 RIVGIAVEQLAYHHDMFIREKCEVAGADCTTGPLYAMVGAACLGVTMTVSLVYIVF 540
QY 572 ELTGGLEYIVLMAAVTSMWGDAGREGIYEAHIRLNGYPLDAKEEFTHTTLADYMR 631
DB 541 ELTGGLEYIVLMAAVTSMWGDAGREGIYEAHIRLNGYPLDAKEEFTHTTLADYMR 600
QY 632 RPRNDPPLAVLTQDMNTVDIENMINETSYNGPPLVMSKESORLVGFALRDLTIAES 691
DB 601 RPRNDPPLAVLTQDMNTVDIENMINETSYNGPPLVMSKESORLVGFALRDLTIAES 660
QY 692 ARKROEGIVSSRVCFAQHPSPSPAESPRPLKLSIIDMSPTVTDHTPMEIYVDIFRKL 751
DB 661 ARKROEGIVSSRVCFAQHPSPSPAESPRPLKLSIIDMSPTVTDHTPMEIYVDIFRKL 720
QY 752 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 791
DB 721 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 760

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RESULT 6
 O9PUI6 PRELIMINARY; PRT: 759 AA.
 ID O9PUI6

AC Q9PUI6; 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Chloride channel CLC-3.
 OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 NC NCBL_TaxID=8127;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99185316; PubMed=10082675;
 RA Miyazaki H., Uchida S., Takai Y., Hirano T., Marumo F., Sasaki S.;
 RT "Molecular cloning of CLC chloride channels in Oreochromis mossambicus
 and their functional complementation of yeast CLC gene mutant.";
 RL Biochem. Biophys. Res. Commun. 255:175-181(1999).
 DR EMBL; AF182215; AAD56388.1; -;
 DR InterPro; IPR000644; CBS_domain.
 DR InterPro; IPR001807; Cl-channel_volt.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00554; voltage_CLC; 1.
 DR PRINTS; PR00762; CLCHANNEL.
 DR SMART; SM00116; CBS; 2.
 SQ SEQUENCE 759 AA; 84752 MW; 63A65CC13GBFD16 CRC64;

Query Match 88.3%; Score 3688.5; DB:13; Length 759;
 Best Local Similarity 90.7%; Pred. No. 2.4e-280;

Matches 690; Conservative 40; Mismatches 29; Indels 3; Gaps 2;

QY 32 MTNGGSI-NSSTHLDLDEPIPGVGYDDPHITDVRRECKDKRHRNRINSKRESAME 90
 DB 1 MSGGGAPSSSTHLDLDEPIPGVGYDDPHITDVRRECKDKRHRNRINSKRESAME 60
 QY 91 MKSLYDANSGLVYTLGLASAGLGLIDIAADMTDLKEGICLSALYNEHCCGWSN 150
 DB 61 FTKNLVDANSGLVYTLGLASAGLGLIDIAADMTDLKEGICLSALYNEHCCGWSN 120
 QY 151 EPTFEERDKCPMKTWAEILIGAEGRGSYIMNYIMYTFWALSFALVSLYVAFAPYAC 210
 DB 121 EPTFAERDKCPMKTWAEILIGAEGRGSYIMNYIMYTFWALSFALVSLYVAFAPYAC 180
 QY 211 GSGIPEIKTLISGFIIRGLYGLKWTLMIKITTLVLAASGLSLEKESPLVHVAOCGGINFS 270
 DB 181 GSGIPEIKTLISGFIIRGLYGLKWTLMIKITTLVLAASGLSLEKESPLVHVAOCGGINFS 240
 QY 271 YLEPKYSTNEAKREVLSAASAGVAVFAPIGVLSLEEVSYYPFLKTIIRSFPAAL 330
 DB 241 YLEPKYSTNEAKREVLSAASAGVAVFAPIGVLSLEEVSYYPFLKTIIRSFPAAL 300
 QY 331 VAAFYRSLINPFGNSRLVFEYEHPTWYLFELFPIILGVFGGLGAPFIRANIMCAR 390
 DB 301 VAAFYRSLINPFGNSRLVFEYEHPTWYLFELFPIILGVFGGLGAPFIRANIMCAR 360
 QY 391 RKSTKRGYVLEVIIVAAITVIAFPNPYTRLNTSELIKELFTDGPLESSSLCYRND 450
 DB 361 RKSTKRGYVLEVIIVAAITVIAFPNPYTRKNTSELIKELFTDGPLESSSLCYRND 420
 QY 451 MAASKIVDIPRPRAGIGYSAIWOLCLALIKRIMTVTFPGIKVNSGLFISMAIGAIA 510
 DB 421 MNGTKAFSD--DOPAGPGVYSAMWOLCLALIKRIMTVTFPGIKVNSGLFISMAIGAIA 478
 QY 511 GRIVGAVPOLAYYHDFWTFKEMCEVGADCTPGIYAVVAAACGAGTBMVSVLVIV 570
 DB 479 GRIVGAVPOLAYYHDFWTFKEMCEVGADCTPGIYAVVAAACGAGTBMVSVLVIV 538
 QY 571 FELTGLEIVPLMAAVMTSKWVGAFRGEGYEAHIRLNGYPPDLDAKEEFTHTTLADY 630
 DB 539 FELTGLEIVPLMAAVMTSKWVGAFRGEGYEAHIRLNGYPPDLDAKEEFTHTTLAREV 598
 QY 631 MRRRNDPLAVLTQDNMTVDIENINETSINGFPVINSKESQRLVGRALRDLTIAIE 690

DB 599 MRRRNDPLAVLTQDNLVLEELQIINETSINGFPVINSKESQRLVGRALRDLTIAIE 658
 QY 691 SARRKQEGIVGSSRVCAQHPSTLPASPPRLKRLSLDMSPTVNDHPMETVIVDFK 750
 DB 659 NARRKQEGIVLSRVYFTQAPPLPADSPPLKRLSLDMSPTVNDHPMETVIVDFK 718
 QY 751 LGRQCLVHNGRLGLITTKDILIRMAOTANODPASIMEN 791
 DB 719 LGRQCLVHNGRLGLITTKDILIRMAOTANODPASIMEN 759

RESULT 7

Q9GKE7 PRELIMINARY; PRT; 746 AA.

AC Q9GKE7; 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Outwardly rectifying chloride channel.
 GN CLC-5.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 NC NCBL_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20545523; PubMed=10978325;
 RA Dowland L.K., Luyckx V.A., Enck A.H., Leclercq B., Yu A.S.L.;
 RT "Molecular Cloning and Characterization of an Intracellular Chloride
 Channel in the Proximal Tubule Cell Line, LLC-PK1.";
 RL J. Biol. Chem. 275:37765-37773(2000).
 DR EMBL; AF274055; AAG29104.1; -;
 DR InterPro; IPR000644; CBS_domain.
 DR InterPro; IPR001807; Cl-channel_volt.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00554; voltage_CLC; 1.
 DR PRINTS; PR00762; CLCHANNEL.
 DR SMART; SM00116; CBS; 2.
 SQ SEQUENCE 746 AA; 83123 MW; 655E3ED45FC61229 CRC64;

Query Match 75.4%; Score 3148.5; DB:6; Length 746;
 Best Local Similarity 76.8%; Pred. No. 1.5e-246;

Matches 574; Conservative 85; Mismatches 87; Indels 1; Gaps 1;

QY 45 LDLDLDEPIPGVGYDDPHITDVRRECKDKRHRNRINSKRESAMTSLYDANSGLV 104
 DB 1 MDLEPIPGVGYDDPHITDVRREKSRDRHREITNSKESMTALHSVDSAFSGWLL 60.
 QY 105 VTLTGLASAGLGLIDIAADMTDLKEGICLSALYNEHCCGWSNETTFFEERDKCPMK 164
 DB 61 MLTIGLSSLAGLIDISAHMMMTDLKEGICTEGLWLNHEHCWNSKHVTEFKDKCPENN 120
 QY 165 TMAELIIGAEGRGSYIMNYIMYTFWALSFALVSLYVAFYACGSGIPEIKTILSGF 224
 DB 121 SMSQLIISADGAFAYIVFMVWALLFAFLAVSLYVAFYACGSGIPEIKTILSGF 180
 QY 225 IIRGYGKWTLMIKITTLVLAASGLSLEKESPLVHVAOCGGINFSYLPKYSTNEAKR 284
 DB 181 IIRGYGKWTLMIKITTLVLAASGLSLEKESPLVHVAOCGGINCHCRKRYRKNNAKR 240
 QY 285 EYLSAASAGVAVFAPIGVLSLEEVSYYPFLKTIIRSFPAALVAAVFLRSINPFGN 344
 DB 241 EYLSAASAGVAVFAPIGVLSLEEVSYYPFLKTIIRSFPAALVAAVFLRSINPFGN 300
 QY 345 SRLVFEYEHPTWYLFELFPIILGVFGGLGAPFIRANIMCARRKSTKRGYVLEY 404
 DB 301 SRLVFEYEHPTWYLFELFPIILGVFGGLGAPFIRANIMCARRKSTKRGYVLEY 360
 QY 405 IIVATVIAFPNPYTRLNTSELIKELFTDGPLESSSLCYRNDMSKIVDIPR 464
 DB 361 LVYATITALLAFNETTRNTSELISELFNDGGLDSSKLCIDYENFNTSKAA-ELPDRP 419
 QY 465 AGIGVSAIWOLCLALIKRIMTVTFPGIKVNSGLFISMAIGAIAIGRIVGAVPOLAYY 524

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Db 420 AGAGVYSAMQALATLLIKIYITFTFGMKIPSGLFIPSMVGAIAAGLLGVCHEQLAY 479
OY 525 HHDFIKEMCEVAGADCTTGGTYAMVGAACLGVTMTVSLVVIYVPELGLGYIYPLM 584
Db 480 HHDAIFNSWCSQGDCTTGGTYAMVGAACLGVTMTVSLVVIYVPELGLGYIYPLM 539
OY 585 AAVMTSKWGDAGFREGIEYEAHRLNGYPLFLDAKEEFTHTTLADVMRPRNDPLAVLT 644
Db 540 AAAMTSKVVADALRGEGYDAHRLNGYPLFLDAKEEFAHKTLAMDVKPRNDPLAVLT 599
OY 645 QDNNVTDDIEMNINETSNGCPVYMSKESQRLVGFALRDLTIAESARKKQEGIVSSR 704
Db 600 QDSMTVEDEVETIISETTYSGFPVVSRESQRLVGFALRDLTIAESARKKQEGIVSTSI 659
OY 705 VCFQOHPTSLPAESPRLKLSILDMSPFTDHTPMEIYVDIFRKGLRCLVTHNGRL 764
Db 660 IYFTHSPMPPTPYPTPLKRLNIDLSFVTDTLPMETIVDIRKGLRCLVTHNGRL 719
OY 765 LGITTKKDLRHHMAQTANODPASIMFN 791
Db 720 LGITTKKDVCLKHIAQMANODPDSILFN 746

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RESULT 8

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O99T03 PRELIMINARY: PRT: 746 AA.
AC O99T03;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chloride channel CLC-5.
OS CLCN5.
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NEW ZEALAND WHITE; TISSUE=CORNEA EPITHELIA;
RL Rae J.L.;
RT "Ion Channels in Cornea Epithelia.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF195523; AAF06018.1;
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl_channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83206 MW; 667F2701C0BF006A CRC64;

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Query Match 75.3%: Score 3145.5; DB 6; Length 746;

Best Local Similarity 77.0%: Pred. No. 2.5e-246; Mismatches 84; Indels 1; Gaps 1;

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OY 45 LDLDDEPIPGVGYDDPFTIDMWREKCDREHRRIRNSKKKESAMETKSLYDAMSGMLV 104
Db 1 MDLFEPIPGVGYDDPFTIDMWREKCDREHRRIRNSKKKESAMETKSLYDAMSGMLV 60
OY 105 VTLTGLASGALAGLIDIAADMTDLKRGICLSALVYHDECOCWGSNETTEERDKCPQWK 164
Db 61 MLTLGLFSGSLAGLIDISAHMTDLKRGICGCFMFHHEHCNMSVNTFEDTDKCPEN 120
OY 165 TWAALLIGAGEGPGSYIMNYIMYIFNALSPFAFLVSLVKVPAPYACSGGIPETITISGF 224
Db 121 SMSOLLINTEGAFAYVNFVYLMALFAFLAVSLVKVPAPYACSGGIPETITISGF 180
OY 225 IIRGYLKMPLMTITLTVLAVASGLSKGKPLVHVAACCGNIFSYLFPYSTNEAKR 284
Db 181 IIRGYLKMPLMTITLTVLAVASGLSKGKPLVHVAACCGNIFSYLFPYSTNEAKR 240
OY 285 EVLSAASAGVSAFAGAPIGGVLFLEEVSYFFPLKTLMSFFAALVAAPVLRISINFGN 344

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Db 241 EYLSAANAAGVSAFAGAPIGGVLFLEEVSYFFPLKTLMSFFAALVAAPVLRISINFGN 300
OY 345 SRLVLFVEYNTPMYLPFLPFIILLGVGGLMGAFPLRANIAMCRKRSTFGGYVPLEV 404
Db 301 SRLVLFVEYNTPMYLPFLPFIILLGVGGLMGAFPLRANIAMCRKRSTFGGYVPLEV 360
OY 405 IIVAITAVIAFPNRYPLNTSELIKELFTDCGPLESSLCDYRNDMAKIVDDIDPR 464
Db 361 LIVAITAIALAFPMRYRMTSELISLNFDCGLDSSKLDENRFTSKGA-DLDRP 419
OY 465 AGIGVSAIWOLCLALFKITIMVFTGIVKPSGLFIPSAIGAIAGIYCIANEOLAY 524
Db 420 AGVGYNAAMQALALIKIYITFTFGMKIPSGLFIPSMVGAIAARLLGVGEOLAY 479
OY 525 HHDFIKEMCEVAGADCTTGGTYAMVGAACLGVTMTVSLVVIYVPELGLGYIYPLM 584
Db 480 HHDAIFNSWCSQGDCTTGGTYAMVGAACLGVTMTVSLVVIYVPELGLGYIYPLM 539
OY 585 AAVMTSKWGDAGFREGIEYEAHRLNGYPLFLDAKEEFTHTTLADVMRPRNDPLAVLT 644
Db 540 AAAMTSKVVADALRGEGYDAHRLNGYPLFLDAKEEFAHKTLAMDVKPRNDPLAVLT 599
OY 645 QDNNVTDDIEMNINETSNGCPVYMSKESQRLVGFALRDLTIAESARKKQEGIVSSR 704
Db 600 QDSMTVEDEVETIISETTYSGFPVVSRESQRLVGFALRDLTIAESARKKQEGIVSTSI 659
OY 705 VCFQOHPTSLPAESPRLKLSILDMSPFTDHTPMEIYVDIFRKGLRCLVTHNGRL 764
Db 660 IYFTHSPMPPTPYPTPLKRLNIDLSFVTDTLPMETIVDIRKGLRCLVTHNGRL 719
OY 765 LGITTKKDLRHHMAQTANODPASIMFN 791
Db 720 LGITTKKDVCLKHIAQMANODPDSILFN 746

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RESULT 9

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O99P66 PRELIMINARY: PRT: 746 AA.
AC O99P66;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chloride channel CLCN5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hysticognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Cornejo I., Cid L.P., Sepulveda F.V.;
RT "Cloning and intestinal expression of guinea pig CLC-5 chloride
channel.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326968; AAG49590.1;
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl_channel_volt.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83093 MW; 92FC8AFDC7D8DA45 CRC64;

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Query Match 74.4%: Score 3109.5; DB 11; Length 746;

Best Local Similarity 76.2%: Pred. No. 2.1e-243; Mismatches 89; Indels 1; Gaps 1;

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OY 45 LDLDDEPIPGVGYDDPFTIDMWREKCDREHRRIRNSKKKESAMETKSLYDAMSGMLV 104
Db 1 MDLFEPIPGVGYDDPFTIDMWREKCDREHRRIRNSKKKESAMETKSLYDAMSGMLV 60
OY 105 VTLTGLASGALAGLIDIAADMTDLKRGICLSALVYHDECOCWGSNETTEERDKCPQWK 164
Db 105 VTLTGLASGALAGLIDIAADMTDLKRGICLSALVYHDECOCWGSNETTEERDKCPQWK 164

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Db 61 MILLILLSCSLAGLIDISAHMMTDLKEGICTEGEMFENHECCWNSOQVTEFDRDKCPEN 120
QY 165 TWAELLIGAEQPGSYIMNYIMYIFWALSFAFLAVSLVAFYACGSGIPEIKTILSGF 224
Db 121 SMSQLINMDEGAFYIVNYEMVIMALLFAFLAVSLVAFYACGSGIPEIKTILSGF 180
QY 225 IIRGYLKWTKITKITTLLAVASGLSLGKESGPLVHVACCNGIFSYLPKYSTNEAKRR 284
Db 181 IIRGYLKWTKITKITTLLAVASGLSLGKESGPLVHVACCNGIFSYLPKYSTNEAKRR 240
QY 285 EYLSAASAGVAVGAPRGVLSLEEVSYPPLKTLRSEFALVAFVLRSTNPECN 344
Db 241 EYLSAASAGVAVGAPRGVLSLEEVSYPPLKTLRSEFALVAFVLRSTNPECN 300
QY 345 SRLVFEYVEHTPMYLFELFPILGVEGGLGAFEFIRANIMCRKRKSTKGYVLEEV 404
Db 301 SRLVFEYVEHTPMYLFELFPILGVEGGLGAFEFIRANIMCRKRKSTKGYVLEEV 360
QY 405 IIVAAITVAVIAPFPNYPLNTSELIKELFTDCGPLLESSSLCDYRNDMAKSTIVDDI 464
Db 361 IIVAAITVAVIAPFPNYPLNTSELIKELFTDCGPLLESSSLCDYRNDMAKSTIVDDI 419
QY 465 AGIGYSAIMOLCLALIKELIMTFTFGIKVPSGLFIPSMAGATAGRVGAVQLAY 524
Db 420 AGIGYSAIMOLCLALIKELIMTFTFGIKVPSGLFIPSMAGATAGRVGAVQLAY 479
QY 525 HHDMFTFKMCEVAGADCTIPGLYAWGAAACLGVTGMTVSLVIVFELTGLLEYVPLM 584
Db 480 HHDMFTFKMCEVAGADCTIPGLYAWGAAACLGVTGMTVSLVIVFELTGLLEYVPLM 539
QY 585 AAVMTSKWVGDAFGREGIYEAHIRLNGYPELDAKEEFTHTTLAADVMRRNDPPLAVLT 644
Db 540 AAVMTSKWVGDAFGREGIYEAHIRLNGYPELDAKEEFTHTTLAADVMRRNDPPLAVLT 599
QY 645 ODNMTVDDIENNINFTSYNGSPVIMSKESQRLVGFALRDLTALIESARKKQEGIVGSSR 704
Db 600 ODNMTVDDIENNINFTSYNGSPVIMSKESQRLVGFALRDLTALIESARKKQEGIVGSSR 659
QY 705 VCFACHTPSLPAESPRLKRLSILMSPPTVDDHTPMEIVDDIFKRLGLRQCLVTHNGRL 764
Db 660 VCFACHTPSLPAESPRLKRLSILMSPPTVDDHTPMEIVDDIFKRLGLRQCLVTHNGRL 719
QY 765 LGITTKKDLIRHMAOTANODPASIMFN 791
Db 720 LGITTKKDLIRHMAOTANODPASIMFN 746

RESULT 10
Q9PMK7 PRELIMINARY: PRT: 808 AA.
AC Q9PMK7.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chloride channel ClC-5.
GN ClC-5.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RC Mo L., Hellmich H.L., Fong P., Wood T.G., Embesi J., Willis N.K.;
RT "Comparison of amphibian and human ClC-5: Similarity of functional
RT properties and inhibition by external pH.";
RL J. Membr. Biol. 186:0-0(1999).
DR EMBL: AF063904; AAD2497.1; -.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR001807; Cl-channel_volt.
DR InterPro: IPR001130; TatD_DNase.
DR Pfam: PF00571; CBS; 2.

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DR Pfam: PF00654; voltage_Clc; 1.
DR PRINTS: PR00762; ClCHANNEL.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS01137; TATD; 1; UNKNOWN; 1.
SQ SEQUENCE 808 AA; 90058 MW; C3F1ADC759BD1676 CRC64;

Query Match 73.8%; Score 3081; DB 13; Length 808;
Best Local Similarity 71.5%; Pred. No. 4.8e-241;
Matches 563; Conservative 105; Mismatches 99; Indels 20; Gaps 3;

QY 22 ELHKRGTHITM-----NGGSINSTHLLDLDEPIRGVGYDFFHTI 64
Db 25 ETETATLDTMTDDVPPIDRDMAAGFVSYNGNLNGAKVMDFLD--VVGYYTEDFNTI 82
QY 65 DWVRECKRREHRRIRNSKKESAMETKSLVDAMSGMLVITLGLASALAGLIDIAAD 124
Db 83 DWVREKSRDRDHRRLSLSKSESTALHSDVADPSGMMLLIGLTASLGLIDISSH 142
QY 125 WMTDLKEGICLSALVYNHQCCWGSNETTFEERDKCPQKWTMAELLIGAEQPGSYIMNY 184
Db 143 WMTDLKEGICLPWFEMFNHQCWNSNNVTFEDRNCPPEWRMSQVLGRSEGAFFYLWY 202
QY 185 IYITWALSFAFLAVSLVAFYACGSGIPEIKTILSGFIIRGYLKWTKITKITTLLV 244
Db 203 IYITWALSFAFLAVSLVAFYACGSGIPEIKTILSGFIIRGYLKWTKITKITTLLV 262
QY 245 AVASGLSLGKESGPLVHVACCNGIFSYLPKYSTNEAKKREYLSAASAGVAVGAPRG 304
Db 263 AVSSGLSLGKESGPLVHVACCNGILCHLTTRKRNKAKREYLSAASAGVAVGAPRG 322
QY 305 GVLFSLEEVSYPPLKTLRSEFALVAFVLRSTNPECNRLVFEYVEHTPMYLFELF 364
Db 323 GVLFSLEEVSYPPLKTLRSEFALVAFVLRSTNPECNRLVFEYVEHTPMYLFELF 382
QY 365 PELLGLGREGGLGAFEFIRANIMCRKRKSTKGYVLEEVIIYAATTAVIAPFPNTN 424
Db 383 PELLGLGREGGLGAFEFIRANIMCRKRKSTKGYVLEEVIIYAATTAVIAPFPNTN 442
QY 425 TSELIKELFTDCGPLLESSSLCDYRNDMAKSTIVDDIPDRPAGIGYSAIMOLCLALIFKI 484
Db 443 SSEMSELFTDCGPLLESSSLCDYRNDMAKSTIVDDIPDRPAGIGYSAIMOLCLALIFKI 501
QY 485 IMTFTFGIKVPSGLFIPSMAGATAGRVGAVQLAYHHDMFTFKMCEVAGADCTIP 544
Db 502 VITFTFGIKVPSGLFIPSMAGATAGRVGAVQLAYHHDMFTFKMCEVAGADCTIP 561
QY 545 GLYAWGAAACLGVTGMTVSLVIVFELTGLLEYVPLMAAVMTSKWVGDAFGREGITE 604
Db 562 GLYAWGAAACLGVTGMTVSLVIVFELTGLLEYVPLMAAVMTSKWVADALGRSTIYD 621
QY 605 AHIRLNGYPELDAKEEFTHTTLAADVMRRNDPPLAVLTODNMVTVDIENNINFTSYNG 664
Db 622 AHIRLNGYPELDAKEEFTHTTLAADVMRRNDPPLAVLTODNMVTVDIENNINFTSYNG 681
QY 665 FPIVVSRESQRLMGVLRDLTALIESARKKQEGIVSTRIYFTEHTPQPTTAPSLKL 741
Db 682 FPIVVSRESQRLMGVLRDLTALIESARKKQEGIVSTRIYFTEHTPQPTTAPSLKL 741
QY 725 RSTLMSPTVDDHTPMEIVDDIFKRLGLRQCLVTHNGRLGLITRKDLIRHMAOTAND 784
Db 742 RAIMDLSPTTIDQTPMEIVDDIFKRLGLRQCLVTHNGRLGLITRKDLIRHMAOTAND 801
QY 785 PASIMFN 791
Db 802 PDSILFN 808

RESULT 11
O13080 PRELIMINARY: PRT: 808 AA.
ID O13080.
AC O13080.
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

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Db 390 AGVGYTTAMMDLALILKRIYTTTFPMKRIJPSGLFIPSMAGAMAGRWGIGVQLAYH 449
OY 525 HHDMFIFKEMCEVAGADCTITPGLYAWGAAACGGVTBMTVSLVIVFELTGLSEIVPLM 584
Db 450 HHDMFIFKEMCEVAGADCTITPGLYAWGAAACGGVTBMTVSLVIVFELTGLSEIVPLM 509
OY 565 AAVMTSKWVGAFREGIYEAHIRLNGYFELDAKEEFTHTTLAADMVBRNDPPLAVLT 644
Db 510 AAAYTSKMWADAFKEGIEYEAHILNGYFELDKDEFTHTRLATDVMRPRGEPLSLVT 569
OY 645 ODMNIVDDIENKINTSYNGFPVIMSKESQRLVGRALRDLTALIESARKKQEGIVGSSR 704
Db 570 QDSMTVEVEVETLIKETDNGEPVLVRSERLIGFQRRELLAKMARQREGIVSNSI 629
OY 705 VCFAGHTSLPAESPRLKSLIDMSPEVTYDHTPMEIVDIFPKLGRCLVTHNGRL 764
Db 630 MYTEPEPELPLANSPLKRLINLSPEYTDHTPMTVVDIFPKLGRCLVTHNGRL 689
OY 765 LGITTKDILRMACTANODPASIMFN 791
Db 690 LGITTKDILRMACTANODPASIMFN 716

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RESULT 13

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O9PUI5 PRELIMINARY; PRT; 840 AA.
AC O9PUI5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Chloride channel CLC-5.
OS Oroschomus mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC Clariidae; Oroschomus.
OC NCBI_TaxID=8127;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=99185316; PubMed=10082675;
RA Miyazaki H., Uchida S., Takel Y., Hirano T., Marumo F., Sasaki S.;
RT "Molecular cloning of CLC chloride channels in Oroschomus mossambicus
RT and their functional complementation of yeast CLC gene mutant.";
RL Biochem. Biophys. Res. Commun. 255:175-181(1999).
DR EMBL; AF182216; AAD56389.1; -.
DR InterPro; IPR000644; CBS domain.
DR InterPro; IPR001807; Cl-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 840 AA; 92293 MW; 81B9996E446F9605 CRC64;

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Query Match 72.6%; Score 3031; DB 13; Length 840;
 Best Local Similarity 71.8%; Pred. No. 5.8e-237;
 Matches 562; Conservative 103; Mismatches 108; Indels 10; Gaps 4;

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OY 16 DNP-----LRELKRRGHTMTNGSINSSTHLLDLEIPGVTGDDHTHDVMEK 70
Db 61 DVPPLSSGVTEH-NGTSRTAGMNGS--GPSRLVDPLEDELPGVGYEDENNTDVAEN 117
OY 71 CKDRRRRRINSKRRESAMENTSLSYDAMSGMLVLTGLASGALAGLIDIAADMVTLK 130
Db 118 SKDRRRRRINSKRRESAMENTSLSYDAMSGMLVLTGLASGALAGLIDIAADMVTLK 177
OY 131 EGCISALAMYNHOCQNSNETTEPERKCPQMTWAELIIGQAGPESYTMNIMYTFW 190
Db 178 GGLCLRGFWNHHCQNSNETTEPERKCPQMTWAELIIGQAGPESYTMNIMYTFW 237
OY 191 ALSEFAVLSVYKFAYPACSGSIPETIILSGFTIRGLKWTLMKTIITLVAVASGL 250
Db 238 ALMSFSLAVIILVAFAPACSGSIPETIILSGFTIRGLKWTLMKTIITLVAVASGL 297

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OY 251 SLGKEGPLVHVACCGNIFSYLEPKYSTNEAKRREVLSAASAGVAFGAPIGVLESL 310
Db 298 SLGKRGPLVHVACCGNIFSYLEPKYSTNEAKRREVLSAASAGVAFGAPIGVLESL 357
OY 311 BEVSYYPFLKTLMRSEFFALVAAPVLRISNPGNSRLVEYVEHTPWYLFELFPFILLG 370
Db 358 BEVSYYPFLKTLMRSEFFALVAAPVLRISNPGNSRLVEYVEHTPWYLFELFPFILLG 417
OY 371 VEGGLMGAFITRANTANORRRKSTFGKYRPLEVYITVAITAVIAFPNRYTLNSELIC 430
Db 418 IFGLMGALFTKANTAMCRLKRTCLGHVPEVLEVVAALTRALLSYPMSTRMSSSELS 477
OY 431 ELFTDCGPLESSLCDDYNDNMASK--IVDDIPDPAGIGVSAIMOLCLALIFKIMTY 488
Db 478 ELFNCSLLDSQGLCYQOPANTSDPGVNSLADRPAGGLCTALAMOLALVEFKMITY 537
OY 489 FTFGIKVPSGLFIPSMAGIAGRIVGTAVEDOLAYVHHDMFIFKEMCEVAGADCTITPGLYA 548
Db 538 ITFGMKVPSGLFIPSMAGIAGRIVGTAVEDOLAYVHHDMFIFKEMCEVAGADCTITPGLYA 597
OY 549 MYGAANACLGVTBMTVSLVIVFELTGLSEIVPLMAAVMTSKWVGAFREGIYEAHIR 608
Db 598 MYGAANACLGVTBMTVSLVIVFELTGLSEIVPLMAAVMTSKWVGAFREGIYEAHIR 657
OY 609 LNGYFELDAKEEFTHTTLAADMVBRNDPPLAVLTODNMVDDIENNI NETSYNGFPVI 668
Db 658 LNGYFELDAKEEFTHTTLAADMVBRNDPPLAVLTODNMVDDIENNI NETSYNGFPVI 717
OY 669 MSKESQRLVGRALRDLTALIESARKKQEGIVGSSRCPAHTPSLPALSPRLKSLIL 728
Db 718 VSESQRLVGRALRDLTALIESARKKQEGIVGSSRCPAHTPSLPALSPRLKSLIL 777
OY 729 DMSPTVTDHTPMEIVDIFPKLGRCLVTHNGRLIGITTKDILRMACTANODPASIM 788
Db 778 DMSPTVTDHTPMEIVDIFPKLGRCLVTHNGRLIGITTKDILRMACTANODPASIM 837
OY 789 MFN 791
Db 838 LFN 840

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RESULT 14

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O9VUY1 PRELIMINARY; PRT; 732 AA.
AC O9VUY1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE CG5284 protein.
DN CG5284.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bokoyeva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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